

SEQUENCE LISTING

<110> Sauter, Margret M.
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTION UNDER HYPOXIC
CONDITIONS

<130> CropDesign

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<141>

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 872

<212> DNA

<213> Rice

<220>

<221> CDS

<222> (69)..(668)

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gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
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Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
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gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
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Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
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115 120 125

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Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
130 135 140

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Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
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His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
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<212> PRT

<213> Rice

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Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly Val Ile
35 40 45
Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
50 55 60
Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
85 90 95

Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
 100 105
 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Ile
 115 120 125
 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
 130 135 140
 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
 145 150 155 160
 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
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 gtctgagagag ttccagag atg gag aac cag ttc cag gat ggc aag gag gag 171
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 1 5 10
 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
 Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
 15 20 25
 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
 Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
 30 35 40
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 Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
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 Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
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 Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
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 Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
 125 130 135

gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603
 Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
 140 145 150 155

gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt 651
 Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
 160 165 170

ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc 699
 Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
 175 180 185

aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcataca 745
 Asn Arg Gly Thr Gln Ala Val Glu Ala Arg
 190 195

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cccgttaaa atctccctga aaatacgcac gtcacatgt cagagtgttt atatacaata 925

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<213> Rice

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 35 40 45
 Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
 50 55 60
 Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
 65 70 75 80
 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
 85 90 95

Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
 100 105
 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
 115 120 125
 Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
 130 135 140
 Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
 145 150 155
 Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
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 Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
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 Gln Ala Val Glu Ala Arg
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<220>
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 <222> (1)..(591)

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 Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
 20 25 30
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 Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
 35 40 45
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 Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
 50 55 60
 gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa 240
 Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
 65 70 75 80
 cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg 288
 Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
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 cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt 336
 His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
 100 105 110

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Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125

ggg gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt 432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

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Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160

att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
165 170 175

gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt 576
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190

aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631
Asn Ala Ala Ala
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aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691

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agtgaattt attatgtgat ttt 774

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<212> PRT

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Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
35 40 45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

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Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
 145 150 155 160
 Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
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 Asn Ala Ala Ala
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 Asp Gln Arg Leu Pro His Gln Lys Asn Pro Glu Phe Val Ser Val 30
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 gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat 143
 Glu Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn 45
 35 40
 gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc 191
 Asp Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly 60
 50 55
 tac agc tac atg gac ttg ctg gat ttg tgc cct gag aag gtg gat aac 239
 Tyr Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn 70 75
 65
 tat gag cag aag ttg aaa aat ttc tat acg gag cac ata cac gca gat 287
 Tyr Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp 90 95
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 gag gag ata cgt tac tgt ctg gaa ggg agt gga tat ttt gat gtg aga 335
 Glu Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg 100 105 110
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 gac aag gat gat cgc tgg att cgc atc tgg atg aag gcc ggt gat atg 383
 Asp Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met 115 120 125
 115
 att gtc ttg cct gct ggg att tac cac cgg ttc acc cta gat act gat 431
 Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp 130 135 140
 130 135 140

aac tat gtc aag ttg atg agg ttg ttt gtg gga gag ccg gtg tgg acg	479
Asn Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr	
145 150 155	
cct tac aat cga cca caa gaa gat cat cca gca agg aag gag tac atc	527
Pro Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile	
160 165 170 175	
aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa	572
Lys Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His	
180 185 190	
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 <212> PRT
 <213> Tomato

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Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn Asp	
35 40 45	
Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly Tyr	
50 55 60	
Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn Tyr	
65 70 75 80	
Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp Glu	
85 90 95	
Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp	
100 105 110	
Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met Ile	
115 120 125	
Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp Asn	
130 135 140	
Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro	
145 150 155 160	
Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile Lys	
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Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His	
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Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
10 15 20

gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tgc ttg 148
Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
25 30 35

gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
40 45 50 55

aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
60 65 70

tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat 292
Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
75 80 85

tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat 340
Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp
90 95 100

gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg 388
Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
105 110 115

gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120 125 130 135

atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc 484
Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
140 145 150

aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act 532
Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
155 160 165

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170 175 180

aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628
Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
185 190 195

gcg taa gatctgggtc tgcctaataca tagtaccaca tgaaaaggac caagactttg 684
Ala
200

ttgctaaagt aagggttgaa aaaaaa gaa taatggtgtc tttaaataaa gggctcctggc 744

ttgttatgcc ttgatgtacc ctgccagtg tttttgtgtc ctgtccctgt ataaagattg 804

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gtatatttat gtaaaaaaaa ataaa 889

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35 40 45
Leu Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala
50 55 60
Asp Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg
65 70 75 80
Gly Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro
85 90 95
Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr
100 105 110
Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val
115 120 125
Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly
130 135 140
Met Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
145 150 155 160
Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp
165 170 175
Thr Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr
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Val Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala
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Thr Ala
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Lys	Arg	Glu	Glu	Val	Ile	Gln	Ala	Trp	Tyr	Met	Asp	Asp	Ser	Asp	Glu	
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gat	cag	agg	ctt	cct	cat	cac	cgt	gaa	cct	aag	gaa	tat	gta	tcc	ttg	149
Asp	Gln	Arg	Leu	Pro	His	His	Arg	Glu	Pro	Lys	Glu	Tyr	Val	Ser	Leu	
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gat	aaa	ctt	gct	gag	ctt	gga	gta	ctc	agc	tgg	cga	ttg	gat	gct	gat	197
Asp	Lys	Leu	Ala	Glu	Leu	Gly	Val	Leu	Ser	Trp	Arg	Leu	Asp	Ala	Asp	
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Asn	Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Glu	Glu	Arg	Gly	
				60					65					70		
tac	tcc	tac	atg	gac	ttc	tgc	gag	gtt	tgc	cct	gag	aag	ctt	cca	aat	293
Tyr	Ser	Tyr	Met	Asp	Phe	Cys	Glu	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn	
			75					80					85			
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Glu	Glu	Ile	Arg	Tyr	Cys	Val	Ala	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	
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gat	cat	aat	gat	aaa	tgg	att	cgt	gtg	tgg	gtg	aag	aaa	gga	ggc	atg	437
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Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	
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Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Asp	Pro	Ile	Trp	Thr	
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Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
170 175 180

aag aac ttt ttg cgg gag gaa ggt ggc caa gcc gtt gat gct gcc 629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gln Ala Val Asp Ala Ala
185 190 195

gca taa aatcaacatt catctgggtgg tggccaagtc gttgatgctg ccgcataaaa 685
Ala
200

tcagcattca tctctgggtat cgtgtctttat aaaatatgaa accccggatt tgtggtaata 745

aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805

ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtattt ctacatttta 865

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<211> 200

<212> PRT

<213> Cotton

<400> 12

Met Thr Met Gly Ser Ala Asp Lys Arg Glu Glu Val Ile Gln Ala Trp
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Tyr Met Asp Asp Ser Asp Glu Asp Gln Arg Leu Pro His His Arg Glu
20 25 30
Pro Lys Glu Tyr Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu
35 40 45
Ser Trp Arg Leu Asp Ala Asp Asn Tyr Glu Asn Asp Glu Glu Leu Lys
50 55 60
Lys Ile Arg Glu Glu Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe
85 90 95
Glu Glu His Ile His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp His Asn Asp Lys Trp Ile Arg Val
115 120 125
Trp Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His
130 135 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Asp Pro Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
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Pro Ala Arg Lys Glu Tyr Ile Lys Asn Phe Leu Arg Glu Glu Gly Gly
180 185 190
Gly Gln Ala Val Asp Ala Ala Ala
195 200

<210> 13
 <211> 919
 <212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (1)..(564)

<400> 13
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 Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
 1 5 10 15

gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc 96
 Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
 20 25 30

gcc cag tgc gct gga gca gct gcg ccg ctc ggg gtg ctc tac tgg aag 144
 Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
 35 40 45

ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga 192
 Leu Asp Ala Asp Lys Tyr Ser Trp Met Asp Pro Glu Leu Glu Lys Ile Arg
 50 55 60

aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat 240
 Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
 65 70 75 80

aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat 288
 Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
 85 90 95

ttg cac ttg gac gat gag atc cgc tac atc ctg gat gcc ser ggg tac 336
 Leu His Leu Asp Asp Glu Ile Arg Tyr Tyr Ile Leu Asp Gly Ser Gly Tyr
 100 105 110

ttc gat gtg agg gac aag gag gac cag tgg atc ccg atc ttc atg gag 384
 Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
 115 120 125

aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg 432
 Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
 130 135 140

gtg gac gag aag aac tac acg aag gcc atg ccg ctg ttt gtg gga gaa 480
 Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
 145 150 155 160

ccg gtg tgg aca gcg tac aac ccg ccc gct gac cat ttt gaa gcc ccg 528
 Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
 165 170 175

ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtctgcc 574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

tggggaactaa cacgtgcctc gtaaaggtcc ccaatgtaat gaactgagca gaaaattcaa 634
tcaactttct ctttgccttt agaggatagc cttgaggtag attatcttcc ctttgtaaga 694
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attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874
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<210> 14

<211> 187

<212> PRT

<213> Human

<400> 14

Arg	Thr	Arg	His	Pro	His	Cys	Ala	Ser	Val	Val	Gln	Ala	Trp	Tyr	Met
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Asp	Asp	Ala	Pro	Gly	Thr	Arg	Gly	Asn	Pro	Thr	Ala	Pro	Thr	Pro	Ala
			20					25					30		
Ala	Gln	Cys	Ala	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Val	Leu	Tyr	Trp	Lys
		35					40					45			
Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys	Ile	Arg
	50					55				60					
Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys	Lys	Asp
	65				70				75					80	
Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Met	Phe	Tyr	Glu	Glu	His
			85					90					95		
Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ser	Gly	Tyr
			100				105					110			
Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp	Gln	Trp	Ile	Arg	Ile	Phe	Met	Glu
			115				120					125			
Lys	Gly	Asp	Met	Val	Thr	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr
			130			135					140				
Val	Asp	Glu	Lys	Asn	Tyr	Thr	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Glu
	145				150					155					160
Pro	Val	Trp	Thr	Ala	Tyr	Asn	Arg	Pro	Ala	Asp	His	Phe	Glu	Ala	Arg
				165				170						175	
Gly	Gln	Tyr	Val	Lys	Phe	Leu	Ala	Gln	Thr	Ala					
			180					185							

cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg 532
Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
160 165 170

agt ttt ttg gaa gga aca gca tag cagtgtctct caaagagaaa actgcactgt 586
Ser Phe Leu Glu Gly Thr Ala
175 180

gtgaatctcc	tgctgttgta	accgaatgga	aagttgctca	ctttctgct	tttgtatttg	646
aacttgaggc	tagactagct	ctctttgcta	ggattgtgag	atcagtgtct	tttaaataaa	706
agcctctcta	aaagtgaagt	ttacatggaa	gccacaaaaa	tgtgaaaaag	tgaccttaat	766
ttccctaac	tgtcaagact	tagaggata	ggagccctgg	attggtatgt	gcattcatgc	826
atggccaatc	ttcatctccc	agatctttag	gtgtctgttg	gtgtgaagct	atgcctcctg	886
caagagggca	gttataacca	gcacaactaa	ccagatgacg	ttttctctct	ttgctgattg	946
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<210> 16

<211> 179

<212> PRT

<213> Mouse

<400> 16

[illegible]

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 170 175 180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct tanacagaca 641

ngcagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701

attat 706

<210> 18

<211> 181

<212> PRT

<213> Zebrafish

<400> 18

Met Ser Val Phe Glu Ala Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp
 1 5 10 15
 Gln Arg Leu Pro His Lys Leu Ser Pro Asn Gln Pro Val Ser Val Gln
 20 25 30
 Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
 35 40 45
 Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
 50 55 60
 Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
 65 70 75 80
 Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
 85 90 95
 Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
 100 105 110
 Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
 115 120 125
 Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
 130 135 140
 Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
 145 150 155 160
 Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
 165 170 175
 Ser Leu Gly Ser Ser
 180